

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: Capon, Daniel J.  
Gregory, Timothy J.

10 (ii) TITLE OF INVENTION: Adheson Variants

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
20 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
30 (B) FILING DATE: 30-JAN-2004  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 10/157,408  
35 (B) FILING DATE: 28-MAY-2002

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/641554  
40 (B) FILING DATE: 17-AUG-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/275310

(B) FILING DATE: 24-MAR-1999

5 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/457918

(B) FILING DATE: 01-JUN-1995

(vii) PRIOR APPLICATION DATA:

10 (A) APPLICATION NUMBER: 08/236311

(B) FILING DATE: 02-MAY-1994

(vii) PRIOR APPLICATION DATA:

15 (A) APPLICATION NUMBER: 07/936190

(B) FILING DATE: 26-AUG-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/842777

(B) FILING DATE: 18-FEB-1992

20 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/250785

(B) FILING DATE: 28-SEP-1988

25 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/104329

(B) FILING DATE: 02-OCT-1987

(viii) ATTORNEY/AGENT INFORMATION:

30 (A) NAME: Kubinec, Jeffrey S.

(B) REGISTRATION NUMBER: 36,575

(C) REFERENCE/DOCKET NUMBER: P0444P1C7

(ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 650/225-8228

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

[illegible]

	Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly	
	170	175 180
5	Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe	
	185	190 195
	Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser Ser Ile	
	200	205 210
10	Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro Leu	
	215	220 225
	Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp	
	230	235 240
15	Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp	
	245	250 255
	Leu Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro	
20	260	265 270
	Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro	
	275	280 285
25	Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala	
	290	295 300
	Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn Leu Val	
	305	310 315
30	Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu Val	
	320	325 330
	Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu	
35	335	340 345
	Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val	
	350	355 360
40		

Leu Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser  
365 370 375

5 Gly Gln Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp  
380 385 390

Ser Thr Pro Ser Phe Asn Ala Val Val Tyr His Ser  
395 400

10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs  
(B) TYPE: Nucleic Acid  
15 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

20

AATTCAAGCC CAGAGCCCTG CCATTTCTGT GGGCTCAGGT CCCTACTGCT 50

CAGCCCCCTTC CTCCTCGGC AAGGCCACAA TGAACCGGGG AGTCCCTTTT 100

25

AGGCACTTGC TTCTGGTGCT GCAACTGGCG CTCCTCCCAG CAGCCACTCA 150

GGGAAACAAA GTGGTGCTGG GCAAAAAAGG GGATACAGTG GAACTGACCT 200

GTACAGCTTC CCAGAAGAAG AGCATACAAT TCCACTGGAA AAACCTCCAAC 250

30

CAGATAAAGA TTCTGGGAAA TCAGGGCTCC TTCTTAACTA AAGGTCCATC 300

CAAGCTGAAT GATCGCGCTG ACTCAAGAAG AAGCCTTTGG GACCAAGGAA 350

35

ACTTTCCCCT GATCATCAAG AATCTTAAGA TAGAAGACTC AGATACTTAC 400

ATCTGTGAAG TGGAGGACCA GAAGGAGGAG GTGCAATTGC TAGTGTTTCGG 450

40

ATTGACTGCC AACTCTGACA CCCACCTGCT TCAGGGGCAG AGCCTGACCC 500

TGACCTTGA GAGCCCCCT GGTAGTAGCC CCTCAGTGCA ATGTAGGAGT 550  
CCAAGGGGTA AAAACATACA GGGGGGGAAG ACCCTCTCCG TGTCTCAGCT 600  
5 GGAGCTCCAG GATAGTGGCA CCTGGACATG CACTGTCTTG CAGAACCAGA 650  
AGAAGGTGGA GTTCAAATA GACATCGTGG TGCTAGCTTT CCAGAAGGCC 700  
TCCAGCATAG TCTATAAGAA AGAGGGGGAA CAGGTGGAGT TCTCCTTCCC 750  
10 ACTCGCCTTT ACAGTTGAAA AGCTGACGGG CAGTGGCGAG CTGTGGTGGC 800  
AGGCGGAGAG GGCTTCCTCC TCCAAGTCTT GGATCACCTT TGACCTGAAG 850  
15 AACAAGGAAG TGTCTGTAAA ACGGGTTACC CAGGACCCTA AGCTCCAGAT 900  
GGGCAAGAAG CTCCCGCTCC ACCTCACCTT GCCCCAGGCC TTGCCTCAGT 950  
ATGCTGGCTC TGGAAACCTC ACCCTGGCCC TTGAAGCGAA AACAGGAAAG 1000  
20 TTGCATCAGG AAGTGAACCT GGTGGTGATG AGAGCCACTC AGCTCCAGAA 1050  
AAATTTGACC TGTGAGGTGT GGGGACCCAC CTCCCCTAAG CTGATGCTGA 1100  
GTTTGAAACT GGAGAACAAG GAGGCAAAGG TCTCGAAGCG GGAGAAGGCG 1150  
GTGTGGGTGC TGAACCCTGA GCGGGGGATG TGGCAGTGTC TGCTGAGTGA 1200  
CTCGGGACAG GTCCTGCTGG AATCCAACAT CAAGGTTCTG CCCACATGGT 1250  
30 CCACCCGAG CTTTAATGCG GTAGTTTATC ACAGTTAAAT TGCTAACGCA 1300  
GTCAGGCACC GTGTATGAAA TCTAACAATG CGCTCATCGT CATCCTCGGC 1350  
35 ACCGTCACCC TGGATGCTGT AGGCATAGGC TTGGTTATGC CGGTACTGCC 1400  
GGGCCTCTTG CGGGAT 1416

(2) INFORMATION FOR SEQ ID NO:3:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 TTAAGTTCGG GTCTCGGGAC GGTAAAGACA CCCGAGTCCA GGGATGACGA 50  
GTCGGGGAAG GAGGGAGCCG TTCCGGTGTT ACTTGGCCCC TCAGGGAAAA 100  
TCCGTGAACG AAGACCACGA CGTTGACCGC GAGGAGGGTC GTCGGTGAGT 150  
15 CCCTTTGTTT CACCACGACC CGTTTTTTCC CCTATGTCAC CTTGACTGGA 200  
CATGTCGAAG GGTCTTCTTC TCGTATGTTA AGGTGACCTT TTTGAGGTTG 250  
20 GTCTATTTCT AAGACCCTTT AGTCCCAGAG AAGAATTGAT TTCCAGGTAG 300  
GTTCGACTTA CTAGCGCGAC TGAGTTCTTC TTCGGAAACC CTGGTTCCTT 350  
TGAAAGGGGA CTAGTAGTTC TTAGAATTCT ATCTTCTGAG TCTATGAATG 400  
25 TAGACACTTC ACCTCCTGGT CTTCTCTCTC CACGTTAACG ATCACAAGCC 450  
TAACTGACGG TTGAGACTGT GGGTGGACGA AGTCCCCGTC TCGGACTGGG 500  
30 ACTGGAACCT CTCGGGGGGA CCATCATCGG GGAGTCACGT TACATCCTCA 550  
GGTTCCCAT TTTTGTATGT CCCCCCTTC TGGGAGAGGC ACAGAGTCGA 600  
CCTCGAGGTC CTATCACCGT GGACCTGTAC GTGACAGAAC GTCTTGGTCT 650  
35 TCTTCCACCT CAAGTTTTAT CTGTAGCACC ACGATCGAAA GGTCTTCCGG 700  
AGGTCGTATC AGATATTCTT TCTCCCCCTT GTCCACCTCA AGAGGAAGGG 750  
40 TGAGCGGAAA TGTCAACTTT TCGACTGCCC GTCACCGCTC GACACCACCG 800

TCCGCCTCTC CCGAAGGAGG AGG TTCAGAA CCTAGTGGAA ACTGGACTTC 850  
TTGTTCTTTC ACAGACATTT TGCCCAATGG GTCCTGGGAT TCGAGGTCTA 900  
5 CCCGTTCTTC GAGGGCGAGG TGGAGTGGGA CGGGGTCCGG AACGGAGTCA 950  
TACGACCGAG ACCTTTGGAG TGGGACCGGG AACTTCGCTT TTGTCCTTTC 1000  
AACGTAGTCC TTCACTTGGA CCACCACTAC TCTCGGTGAG TCGAGGTCTT 1050  
10 TTTAAACTGG ACACTCCACA CCCCTGGGTG GAGGGGATTC GACTACGACT 1100  
CAAAC TTTGA CCTCTTGTTT CTCCGTTTCC AGAGCTTCGC CCTCTTCCGC 1150  
CACACCCACG ACTTGGGACT CCGCCCCTAC ACCGTCACAG ACGACTCACT 1200  
15 GAGCCCTGTC CAGGACGACC TTAGGTTGTA GTTCCAAGAC GGGTGTACCA 1250  
GGTGGGGCTC GAAATTACGC CATCAAATAG TGTCAATTTA ACGATTGCGT 1300  
20 CAGTCCGTGG CACATACTTT AGATTGTTAC GCGAGTAGCA GTAGGAGCCG 1350  
TGGCAGTGGG ACCTACGACA TCCGTATCCG AACCAATACG GCCATGACGG 1400  
25 CCCGGAGAAC GCCCTA 1416

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 434 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35 Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val  
1 5 10 15  
Val Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala  
40 20 25 30



40

	Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser	
	230	235 240
5	Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe	
	245	250 255
	Pro Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu	
	260	265 270
10	Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr	
	275	280 285
	Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln	
	290	295 300
15	Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr	
	305	310 315
	Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr	
20	320	325 330
	Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn	
	335	340 345
25	Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys	
	350	355 360
	Glu Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys	
	365	370 375
30	Leu Glu Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val	
	380	385 390
	Trp Val Leu Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser	
35	395	400 405
	Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro	
	410	415 420
40		

Thr Trp Ser Thr Pro Ser Phe Asn Ala Val Val Tyr His Ser  
425 430

(2) INFORMATION FOR SEQ ID NO:5:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1508 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15

AAGCTTCAGC GCGAACGACC AACTACCCCG ATCATCAGTT ATCCTTAAGG 50

TCTCTTTTGT GTGGTGC GTT CCGGTATGGG GGGGACTGCC GCCAGGTTGG 100

GGGCCGTGAT TTTGTTTGTC GTCATAGTGG GCCTCCATGG GGTCCGCGGC 150

20

AAATATGCCT TGGCGGATGC CTCCTCAAG ATGGCCGACC CCAATCGATT 200

TCGCGGCAAA GACCTTCCGG TCCTGGACCA GCTGCTCGAG CAGGGAAACA 250

25

AAGTGGTGCT GGGCAAAAAA GGGGATACAG TGGAAGTGAC CTGTACAGCT 300

TCCCAGAAGA AGAGCATACA ATTCCACTGG AAAAAGTCCA ACCAGATAAA 350

GATTCTGGGA AATCAGGGCT CCTTCTTAAC TAAAGGTCCA TCCAAGCTGA 400

30

ATGATCGCGC TGAAGCAAGA AGAAGCCTTT GGGACCAAGG AACTTTTCCC 450

CTGATCATCA AGAATCTTAA GATAGAAGAC TCAGATACTT ACATCTGTGA 500

35

AGTGGAGGAC CAGAAGGAGG AGGTGCAATT GCTAGTGTTT GGATTGACTG 550

CCAACTCTGA CACCCACCTG CTCAGGGGAC AGAGCCTGAC CCTGACCTTG 600

GAGAGCCCCC CTGGTAGTAG CCCCTCAGTG CAATGTAGGA GTCCAAGGGG 650

40

TAAAAACATA CAGGGGGGGA AGACCCTCTC CGTGTCTCAG CTGGAGCTCC 700  
AGGATAGTGG CACCTGGACA TGCACGTGTCT TGCAGAACCA GAAGAAGGTG 750  
5 GAGTTCAAAA TAGACATCGT GGTGCTAGCT TTCCAGAAGG CCTCCAGCAT 800  
AGTCTATAAG AAAGAGGGGG AACAGGTGGA GTTCTCCTTC CCACTCGCCT 850  
TTACAGTTGA AAAGCTGACG GGCAGTGGCG AGCTGTGGTG GCAGGCGGAG 900  
10 AGGGCTTCCT CCTCCAAGTC TTGGATCACC TTTGACCTGA AGAACAAGGA 950  
AGTGTCTGTA AAACGGGTTA CCCAGGACCC TAAGCTCCAG ATGGGCAAGA 1000  
15 AGCTCCCGCT CCACCTCACC CTGCCCCAGG CTTGCCTCA GTATGCTGGC 1050  
TCTGGAAACC TCACCCTGGC CTTGAAGCG AAAACAGGAA AGTTGCATCA 1100  
GGAAGTGAAC CTGGTGGTGA TGAGAGCCAC TCAGCTCCAG AAAAATTGTA 1150  
20 CCTGTCAGGT GTGGGGACCC ACCTCCCCTA AGCTGATGCT GAGTTTGAAA 1200  
CTGGAGAACA AGGAGGCAAA GGTCTCGAAG CGGGAGAAGG CGGTGTGGGT 1250  
25 GCTGAACCCT GAGGCGGGGA TGTGGCAGTG TCTGCTGAGT GACTCGGGAC 1300  
AGGTCTTGCT GGAATCCAAC ATCAAGGTTC TGCCACATG GTCCACCCCG 1350  
AGCTTTAATG CGGTAGTTTA TCACAGTTAA ATTGCTAACG CAGTCAGGCA 1400  
30 CCGTGTATGA AATCTAACA TGCCTCATC GTCATCCTCG GCACCGTCAC 1450  
CCTGGATGCT GTAGGCATAG GCTTGGTTAT GCCGGTACTG CCGGGCCTCT 1500  
35 TGCGGGAT 1508

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1508 base pairs

(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
TTCGAAGTCG CGCTTGCTGG TTGATGGGGC TAGTAGTCAA TAGGAATTCC 50
10 AGAGAAAACA CACCACGCAA GGCCATACCC CCCCTGACGG CGGTCCAACC 100
    CCCGGCACTA AAACAAACAG CAGTATCACC CGGAGGTACC CCAGGCGCCG 150
    TTTATACGGA ACCGCCTACG GAGAGAGTTC TACCGGCTGG GGTTAGCTAA 200
15 AGCGCCGTTT CTGGAAGGCC AGGACCTGGT CGACGAGCTC GTCCCTTTGT 250
    TTCACCACGA CCCGTTTTTT CCCCTATGTC ACCTTGACTG GACATGTCGA 300
20 AGGGTCTTCT TCTCGTATGT TAAGGTGACC TTTTGTAGGT TGGTCTATTT 350
    CTAAGACCCT TTAGTCCCGA GGAAGAATTG ATTTCCAGGT AGGTTCGACT 400
    TACTAGCGCG ACTGAGTTCT TCTTCGAAA CCCTGGTTCC TTTGAAAGGG 450
25 GACTAGTAGT TCTTAGAATT CTATCTTCTG AGTCTATGAA TGTAGACACT 500
    TCACCTCCTG GTCTTCCTCC TCCACGTAA CGATCACAAG CCTAACTGAC 550
30 GGTGAGACT GTGGGTGGAC GAAGTCCCCG TCTCGGACTG GGACTGGAAC 600
    CTCTCGGGGG GACCATCATC GGGGAGTCAC GTTACATCCT CAGGTTCCCC 650
    ATTTTTGTAT GTCCCCCCT TCTGGGAGAG GCACAGAGTC GACCTCGAGG 700
35 TCCTATCACC GTGGACCTGT ACGTGACAGA ACGTCTTGGT CTTCTTCCAC 750
    CTCAAGTTTT ATCTGTAGCA CCACGATCGA AAGGTCTTCC GGAGGTCGTA 800
40 TCAGATATTC TTTCTCCCC TTGTCCACCT CAAGAGGAAG GGTGAGCGGA 850
```

AATGTCAACT TTTCGACTGC CCGTCACCGC TCGACACCAC CGTCCGCCTC 900  
 TCCCGAAGGA GGAGGTTCAG AACCTAGTGG AACTGGACT TCTTGTTTCCT 950  
 5 TCACAGACAT TTGCCCCAAT GGGTCCTGGG ATTCGAGGTC TACCCGTTCT 1000  
 TCGAGGGCGA GGTGGAGTGG GACGGGGTCC GGAACGGAGT CATACGACCG 1050  
 AGACCTTTGG AGTGGGACCG GGAACCTTCGC TTTTGTCTT TCAACGTAGT 1100  
 10 CCTTCACTTG GACCACCACT ACTCTCGGTG AGTCGAGGTC TTTTAACT 1150  
 GGACACTCCA CACCCCTGGG TGGAGGGGAT TCGACTACGA CTCAAACCTT 1200  
 15 GACCTCTTGT TCCTCCGTTT CCAGAGCTTC GCCCTCTTCC GCCACACCCA 1250  
 CGACTTGGA CTCCGCCCCCT ACACCGTCAC AGACGACTCA CTGAGCCCTG 1300  
 TCCAGGACGA CCTTAGGTTG TAGTTCCAAG ACGGGTGATC CAGGTGGGGC 1350  
 20 TCGAAATTAC GCCATCAAAT AGTGTCAATT TAACGATTGC GTCAGTCCGT 1400  
 GGCACATACT TTAGATTGTT ACGCGAGTAG CAGTAGGAGC CGTGGCAGTG 1450  
 25 GGACCTACGA CATCCGTATC CGAACCAATA CGGCCATGAC GGCCCGGAGA 1500  
 ACGCCCTA 1508

(2) INFORMATION FOR SEQ ID NO:7:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Thr  
 1 5 10 15

40

	Phe Cys Leu Trp Tyr Arg Glu Arg Pro Pro Cys Trp Ile Asp Pro	
	20	25 30
5	Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys	
	35	40 45
	Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser	
	50	55 60
10	Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro	
	65	70 75
	Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly	
	80	85 90
15	Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
	95	100 105
	Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln	
20	110	115 120
	Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
	125	130 135
25	Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys	
	140	145 150
	Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe	
	155	160 165
30	Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	
	170	175 180
	Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro	
35	185	190 195
	Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn	
	200	205 210
40		

	Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg	
	215	220 225
5	Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
	230	235 240
	Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
	245	250 255
10	Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
	260	265 270
	Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
	275	280 285
15	Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
	290	295 300
	Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	
20	305	310 315
	Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu	
	320	325 330
25	Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
	335	340 345
	Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr	
	350	355 360
30	Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
	365	370

(2) INFORMATION FOR SEQ ID NO:8:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1135 base pairs
	(B) TYPE: Nucleic Acid
	(C) STRANDEDNESS: Single
40	(D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
5      GAATTCTGTC ACTGCCGCGG ACACGGCCGT ATATTACTGT GCGAGAGCCA 50
      CCTTTTGCCT ATGGTACAGG GAGCGTCCCC CTTGTTGGAT CGACCCCTGG 100
      GGCCTGGGAA CCCTGGTCAC CGTCTCCTCG GCCTCCACCA AGGGCCCATC 150
10     GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG GGCACAGCGG 200
      CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 250
      TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT 300
15     ACAGTCCTCA GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA 350
      GCAGCTTGGG CACCCAGACC TACATCTGCA ACGTGAATCA CAAGCCCAGC 400
20     AACACCAAGG TGGACAAGAA AGTTGAGCCC AAATCTTGTG AAAAACTCA 450
      CACATGCCCC CCGTGCCCAG CACCTGAACT CCTGGGGGGA CCGTCAGTCT 500
      TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 550
25     GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA 600
      GTTCAAGTGG TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC 650
30     CGCGGGAGGA GCAGTACAAC AGCACGTACC GGGTGGTCAG CGTCCTCACC 700
      GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT GCAAGGTCTC 750
      CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC AAAGCCAAAG 800
35     GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 850
      CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC 900
40     CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC 950
```

ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTCCTCTAC 1000  
AGCAAGCTCA CCGTGGACAA GAGCAGGTGG CAGCAGGGGA ACGTCTTCTC 1050  
5 ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG CAGAAGAGCC 1100  
TCTCCCTGTC TCCGGGTAAA TGAGTGCACG GGCCG 1135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTAAGACAG TGACGGCGCC TGTGCCGGCA TATAATGACA CGCTCTCGGT 50  
GGAAAACGGA TACCATGTCC CTCGCAGGGG GAACAACCTA GCTGGGGACC 100  
CCGGACCCTT GGGACCAGTG GCAGAGGAGC CGGAGGTGGT TCCCGGGTAG 150  
25 CCAGAAGGGG GACCGTGGGA GGAGGTTCTC GTGGAGACCC CCGTGTCGCC 200  
GGGACCCGAC GGACCAGTTC CTGATGAAGG GGCTTGGCCA CTGCCACAGC 250  
ACCTTGAGTC CGCGGGACTG GTCGCCGCAC GTGTGGAAGG GCCGACAGGA 300  
TGTCAGGAGT CCTGAGATGA GGGAGTCGTC GCACCACTGG CACGGGAGGT 350  
CGTCGAACCC GTGGGTCTGG ATGTAGACGT TGCACTTAGT GTTCGGGTCG 400  
35 TTGTGGTTCC ACCTGTTCTT TCAACTCGGG TTTAGAACAC TGTTTTGAGT 450  
GTGTACGGGT GGCACGGGTC GTGGACTTGA GGACCCCCCT GGCAGTCAGA 500  
40 AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG GGCCTGGGGA 550

CTCCAGTGTA CGCACCACCA CCTGCACTCG GTGCTTCTGG GACTCCAGTT 600  
CAAGTTGACC ATGCACCTGC CGCACCTCCA CGTATTACGG TTCTGTTTCG 650  
5 GCGCCCTCCT CGTCATGTTG TCGTGCATGG CCCACCAGTC GCAGGAGTGG 700  
CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA CGTTCCAGAG 750  
GTTGTTTTCGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG TTTCGGTTTC 800  
10 CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG GGCCCTACTC 850  
GACTGGTTCT TGGTCCAGTC GGACTGGACG GACCAGTTTC CGAAGATAGG 900  
15 GTCGCTGTAG CGGCACCTCA CCCTCTCGTT ACCCGTCGGC CTCTTGTTGA 950  
TGTTCTGGTG CGGAGGGCAC GACCTGAGGC TGCCGAGGAA GAAGGAGATG 1000  
TCGTTGAGT GGCACCTGTT CTCGTCCACC GTCGTCCCCT TGCAGAAGAG 1050  
20 TACGAGGCAC TACGTACTAC GTACTCCGAG ACGTGTGGT GATGTGCGTC 1100  
TTCTCGGAGA GGGACAGAGG CCCATTTACT CACGCTGCCG GC 1142

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
(B) TYPE: Amino Acid  
30 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Phe Ala Thr Tyr  
35 1 5 10 15  
Tyr Cys Gln Gln Tyr Lys Ser Leu Ser Leu Thr Phe Gly Gly Gly  
20 25 30

40

[illegible]

25 (2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 468 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35  
GAATTCACTC TCACCATCAG CGGCCTGCAG CCTGAAGATT TTGCAACTTA 50  
TTACTGCCAA CAGTATAAGA GTTTGTCTGCT CACTTTCGGC GGAGGGACCA 100  
40  
AGGTGGAGAT CAAACGAACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 150

CCATCTGATG AGCAGTTGAA ATCTGGA ACT GCCTCTGTTG TGTGCCTGCT 200  
GAATAACTTC TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG 250  
5 CCCTCCAATC GGGTAACTCC CAGGAGAGTG TCACAGAGCA GGACAGCAAG 300  
GACAGCACCT ACAGCCTCAG CAGCACCTG ACGCTGAGCA AAGCAGACTA 350  
CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG GGCCTGAGCT 400  
10 CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGTTAGAG GGAGAAGTGC 450  
CCCCACCTGC TCCTCAGT 468

15 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 468 base pairs  
(B) TYPE: Nucleic Acid  
20 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25 CTTAAGTGAG AGTGGTAGTC GCCGGACGTC GGACTTCTAA AACGTTGAAT 50  
AATGACGGTT GTCATATTCT CAAACAGCGA GTGAAAGCCG CCTCCCTGGT 100  
30 TCCACCTCTA GTTTGCTTGA CACCGACGTG GTAGACAGAA GTAGAAGGGC 150  
GGTAGACTAC TCGTCAACTT TAGACCTTGA CGGAGACAAC ACACGGACGA 200  
CTTATTGAAG ATAGGGTCTC TCCGGTTTCA TGTCACCTTC CACCTATTGC 250  
35 GGGAGGTTAG CCCATTGAGG GTCCTCTCAC AGTGTCTCGT CCTGTCGTTC 300  
CTGTCTGGA TGTCGGAGTC GTCGTGGGAC TGCGACTCGT TTCGTCTGAT 350  
40 GCTCTTTGTG TTTCAGATGC GGACGCTTCA GTGGGTAGTC CCGGACTCGA 400

GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC TCACAATCTC CCTCTTCACG 450

GGGGTGGACG AGGAGTCA 468

5 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: Nucleic Acid

10 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15

AATTCAAGCC CAGAGCCCTG CCATTTCTGT GGGCTCAGGT CCCT 44

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTGCTCAGC CCCTTCCTCC CTCGGCAAGG CCACAATGAA CCGGGGAGTC 50

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: Nucleic Acid

35 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

40

CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA CTGGCGCTCC TCCCAGC 47

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGCCACTCAG GGAAACAAAG TGGTGCTGGG CAAAAAAGGG GATACAGTGG 50

15

AACTGACCTG T 61

(2) INFORMATION FOR SEQ ID NO:17:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACAGGTCAGT TCCACTGTAT CCCCTTTTTT GCCCAGCACC ACTTTGTTTC 50

30

C 51

(2) INFORMATION FOR SEQ ID NO:18:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGAGTGGCT GCTGGGAGGA GCGCCAGTTG CAGCACCAGA AGCAAGT 47

5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 50 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15

GCCTAAAAGG GACTCCCCGG TTCATTGTGG CCTTGCCGAG GGAGGAAGGG 50

(2) INFORMATION FOR SEQ ID NO:20:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

25

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

GCTGAGCAGT AGGGACCTGA GCCCACAGAA ATGGCAGGGC TCTGGGCTTG 50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 59 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:



CTGCTCGAGC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG GGGATACAGT 50

GGAAGTAC 59

5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 59 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

15

ACAGGTCAGT TCCACTGTAT CCCCTTTTTT GCCCAGCACC ACTTTGTTTC 50

CCTGCTCGA 59

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 21 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30

CGTGATAGAA GCTTTCTAGA G 21

(2) INFORMATION FOR SEQ ID NO:24:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCCTTTTTTG CCCAGCACCA CCTTCTTGCC CTGAGTGGCT GCTGGGAGGA 50

5

G 51

(2) INFORMATION FOR SEQ ID NO:25:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCACCTTCTT GCCCTG 16

20

25